## IAP20 Rec'd PC+/PTO 393302006

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## IAP20 Rec'd PCT/PTO J 9 JUN 2006

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65	70	75	80
Glu Lys Phe Arg Gly 85	Lys Thr Thr Leu	Thr Ala Asp Lys	Ser Ser Ser 95
Thr Ala Tyr Ile Leu 100	Leu Ser Ser Leu 105		Ser Ala Met 110
Tyr Phe Cys Val Arg	Ser Asp Asp Phe	Asp Tyr Trp Gly	Gln Gly Thr
Thr Leu Thr Val Ser	Ser		
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Met His Phe Gln Val	. Gln lle Phe Sei		
1 5		10	15
gtc atc atg tcc aga	gga caa att gtt	ctc acc cag tcg c	ca gca atc 96
Val Ile Met Ser Arg			
20	25		30
atg tct gca tct cca			
Met Ser Ala Ser Pro	o Gly Glu Lys Val	l Thr Ile Thr Cys	Ser Ala Ser

tca agt gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro act cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile age ega atg gag get gaa gat get gee aet tat tae tge eag eaa agg Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg acg agt tat cca ccc acg ttc ggc tcg ggg aca aag ttg gag ata aaa Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys <210> <211> <212> PRT <213> Mus musculus <400> Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile 

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser

Ser	Ser 50	Val	Ser	Tyr	Met	His 55	Trp	Phe	Gln	Gln	Lys 60	Pro	Gly	Thr	Phe	
Pro 65	Lys	Leu	Trp	Ile	Tyr 70	Ser	Thr	Ser	Asn	Leu <sup>*</sup> 75	Ala	Ser	Gly	Val	Pro 80	
Thr	Arg	Phe	Ser	Gly 85	Ser	Gly	Ser	Gly	Thr 90	Ser	Tyr	Ser	Leu	Thr 95	Ile	
Ser	Arg	Met	Glu 100	Ala	Glu	Asp	Ala	Ala 105	Thr	Tyr	Tyr	Cys	Gln 110	Gln	Arg	
Thr	Ser	Tyr 115	Pro	Pro	Thr	Phe	Gly 120	Ser	Gly	Thr	Lys	Leu 125	Glu	Ile	Lys	-
														٠.		
/91/	ns.	13														
<210 <21		13 792													•	
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<22	2>	(1)	(79	2)												
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_		tgg														48
Met	Arg	Trp	Ser		Ile	Phe	Leu	Phe		Leu	Ser	· Ile	Thr		Gly	
1				5		•			10					15		
		+	007	at a	00~	++~	007	002	t a t	<b>.</b>	oot i		nta n	rta o	12 a	96
_		tgc													Lys	30
val	nis	Cys	20	, al	GIII	ren	0111	25	961	Oly	110	, 010	30		. Lys	
								20								

			Met	tgt a Cys			Ser				144
		His		aaa c Lys		Arg	•		•		192
				gga g Gly	Asp				Tyr		240
				ctg a Leu				Ser		•	288
_				ctg a Leu 105							336
				ttt g Phe							384
	_			ggc g							432
Gly				ctc a							480
				acc a				_		ca Ser	528

agt gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro 180 185 190	576
aaa ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct act Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr 195 200 205	624
cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser 210 215 220	672
cga atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg acg Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr 225 230 235 240	720
agt tat cca ccc acg ttc ggc tcg ggg aca aag ttg gag ata aaa gac Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp 245 250 255	768
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Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys 20 25 30	

Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			

- Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu 50 55 60
- Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn 65 70 75 80
- Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Ser Ser 90 95
- Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met 100 105 110
- Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
  115 120 125
- Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser 130 135 140
- Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met 145 150 155 160
- Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser 165 170 175
- Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro 180 185 190
- Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr 195 200 205
- Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser 210 215 220

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr 225 230 235 240 Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp 245 250 255 Tyr Lys Asp Asp Asp Lys 260 <210> 15 <211> 35 <212> DNA <213> Artificial <220> <223> an artificially synthesized primer sequence <400> 15 Cctgaattcc accatgcgat ggagctggat ctttc 35 <210> 16 <211> 48 <212> DNA <213> Artificial <220> an artificially synthesized primer sequence 16 <400> accgccagag ccacctccgc ctgaaccgcc tccacctgag gagactgt 48

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gaa		03
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⟨223⟩	an artificially synthesized primer sequence	•
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cccgag	cc	68